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Sequence 6913, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Duclert, A.:
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.022.RE
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1909-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6913
LENGTH: 68
                                                               Sequence 516, Requence 516, Sequence 516, Sequence 516, Sequence 516, Sequence 516, Sequence 516, Requence 516, Re
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PPQR--NSFFIIYLFNNRDEVSPCCPGWCQSPGLKQSICPGSPKCWDYCRKPP
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILITATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 57036
LENGTH: 836
PCT-USO2-32727-17586
US-10-131-8134-516
US-10-131-8134-516
US-10-131-824A-516
US-10-131-824A-516
US-10-131-824A-516
US-10-131-824A-516
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US-10-128-814-516
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US-10-131-833A-516
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US-10-131-833A-516
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Pred. No. 0.098;
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Pred. No. 23;
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ORGANISM: Homo sapiens
US-09-724-676-57036
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US-09-513-999C-6913
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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Sequence 57036, A
Sequence 57039, A
Sequence 57039, A
Sequence 57041, A
Sequence 57071, A
Sequence 57071, A
Sequence 57071, A
Sequence 57073, A
Sequence 57074, A
Sequence 57074, A
Sequence 57077, A
Sequence 57077, A
Sequence 57111, A
Sequence 57114, A
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155.522 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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Compugen Ltd.
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US-09-724-676-53564
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                          GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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US-09-724-676-57041
US-09-724-676-57041
Sequence 57041, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 57041
                                                                                                                                                                                                                                                                                                APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 57040
LENGTH: 836
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
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4; Mismatches
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Pred. No.
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Pred. No.
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                                                        19.8%;
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illarity 32.4%;
Conservative
                                                      Query Match 19.8°
Best Local Similarity 32.4°
Matches 11; Conservative
   ; ORGANISM: Homo sapiens
US-09-724-676-57039
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US-09-724-676-57040
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CORGANISM: Homo sapiens
US-09-724-676-57041
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Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
Matches 11; Conserv
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US-09-724-676-57040
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57037
LENGTH: 836
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVERTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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Pred. No. 23;
4; Mismatches 1
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23;
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 Mismatches
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                                  3 RONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWA 36
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Pred. No.
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32.4%;
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Best'Local Similarity 32.4%;
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Matches 11; Conservative
Conservative
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US-09-724-676-57038
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US-09-724-676-57037
                                                                                                                             RESULT<sub>1</sub> 3
US-09-724-676-57037
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LENGTH: 836
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LENGTH: 836
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Length 836;
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57075
LENGTH: 836
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
APPLICANT: COMPUGEN LTD
TITLE OF INVENTION: Variants of alternative splicing
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                                                                                                                                                                                                                                                               Score 57; DB 5;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%; Score 57; DB 5; 32.4%; Pred. No. 23; tive 4; Mismatches 1
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO.55077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-724-676-57075
; Sequence 57075, Application US/09724676
; GENERAL INFORMATION:
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ilarity 32.4%;
Conservative
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Best Local Similarity 32.4%;
Matches 11; Conservative
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Best Local Similarity 32.4%;
Matches 11; Conservative
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US-09-724-676-57077
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US-09-724-676-57074
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Best Local Similarity
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US-09-724-676-57077
                                                                                                                                             SEQ ID NO 57074
LENGTH: 836
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Pred. No. 23;
4; Mismatches 19; Indels
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23;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD:
TTYLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57073
TYPE: PRT
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57072
LENGTH: 836
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US-09-724-676-57072
; Sequence 57072, Application US/09724676
; GENERAL INFORMATION:
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                     SOFTWARE: PatentIn version 3.2
SEQ ID NO 57071
LENGTH: 836
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Best Local Similarity 32.4%;
Matches 11; Conservative
  NUMBER OF SEQ ID NOS: 97222
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US-09-724-676-57073
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US-09-724-676-57073
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US-09-724-676-57074
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Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels
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Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels
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US-09-724-676-57110

S Equence 57110, Application US/09724676

GENERAL INFORMATION:
TITLE OF INVENTION: VALENTS of alternative splicing;
FILE REFERENCE: 122181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

SOFTWARE: PatentIn version 3.2

SEQ ID NO 57110

TYPE: PRT
RESULT 14
US-09-724-676-57108
Sequence 57108, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing; FIJE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57108
LENGTH: 836
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ORGANISM: Homo sapiens
US-09-724-676-57108
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US-09-724-676-57110
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Search completed: November 22, 2002, 14:30:05 Job time : 12 secs

Sequence 2, Appli

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1 KQRQNKPPSKPNNDFHFEVF.......NNPTCWALCKRIPNKKPGKK
                         GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli	Sequence 32, Appl	Sequence 36, Appl	Sequence 40, Appl	Sequence 42, Appl	Sequence 43, Appl
SUMMARIES	QI	US-09-202-035-1	US-09-202-035-32	US-09-202-035-36	US-09-202-035-40	US-09-202-035-42	US-09-202-035-43
	DB	16	16	16	16	16	16
	Query Match Length DB	49	49	49	49	49	49
d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0
	Score	288	288	288	288	288	288
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7-107-007-00-cn	US-09-202-035-2 US-09-202-035-3	US-09-202-035-5	US-09-202-033-6 US-09-202-035-7	US-09-202-035-8	US-09-647-309A-38.	US-09-462-918C-43	US-09-647-309A-4	US-10-088-720-9	US-08-896-442-4	US-09-272-262-4 US-09-462-816-4	US-08-344-639-8	US-08-344-639A-8	US-08-344-639C-8	US-08-344-639D-8 US-08-467-961-8	US-08-467-963-8	US-08-467-963B-8	US-US-40/-909-8 US-08-834-204-8	US-08-838-189-8	US-08-838-189A-8	US-08-838-189B-8	US-08-838-189C-8	US-U8-838-189D-8 US-08-850-344-8	US-08-852-344A-8	US-08-852-344B-8	US-08-852-344C-8	US-U8-896-442-2 US-09-272-262-2	US-09-462-816-2	8 US-09-479-240-8 4 US-10-088-720-4	ALIGNMENTS		15-09-202-035-1	02035	ď	tides with Structural	ry syncytiai virus	8/09/202,035	17	CT/AU97/00351 04	U PO 0265	05					ial virus	; Score 288; DB 1 ; Pred. No. 1e-25;	0	KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK		
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				<i>)</i>																								44 285 45 285			-09-202-035-1	equence 1, A	APPLICANT: J	TITLE OF INV	TITLE OF INV	CURRENT APPL	CURRENT FILI	EARLIER APPL FAPLIER FILT	EARLIER APPL	EARLIER FILI	NUMBER OF SE	SOFTWAKE: PA	LENGTH:	PRT	ORGANISM: r 09-202-035-1	Query Match Best Local Si	4	1 KORON	1 KQRQN	
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ORGANISM: respiratory syncytial virus
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Sequence 40, Application US/09202035 GENERAL INFORMATION:
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ilarity 100.0%; P
Conservative 0;
                                              APPLICANT: Jeffrey John Gorman
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; OTHER INFORMATION: amidation
US-09-202-035-42
                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 49
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Best Local Similarity
Matches 49; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                     APPLICANT: Jeffrey John Gorman
TIȚLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TIȚLE OF INVENTION: Respiratory Syncytial Virus
TIŢLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER PILING DATE: 1997-06-04
EARLIER PILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 44
SCPTWARE: Patentin Ver. 2.1
SEQ IID NO 32
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TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER PILING DATE: 1998-12-17
EARLIER FILING DATE: 1990-06-05
EARLIER FILING DATE: 1990-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 36, Application US/09202035; GENERAL INFORMATION:
                                                              Sequence 32, Application US/09202035 GENERAL INFORMATION:
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OTHER INFORMATION: acetylation
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Matches 49; Conservative
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Matches 49; Conser
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US-09-202-035-36
                                         us-09-202-035-32
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RESULT: 4 <u>उ</u>

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APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 41582000100
CURRENT PAPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER FILING DATE: 1998-12-17
EARLIER FILING DATE: 1996-06-04
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
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TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of TITLE OF INVENTION: Respiratory Syncytial Virus FILLE REPREBNE: 41585200100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER PILING DATE: 1997-06-04
EARLIER FILING DATE: 1997-06-04
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
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OTHER INFORMATION: benzoyl benzylamide derivatisation
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Pred. No. 1e-25;
; Mismatches 0;
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Sequence 3, Application US/09202035

Sequence 3, Application US/09202035

GENERAL INFORMATION:
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER FILING DATE: 1998-12-17
EARLIER FILING DATE: 1997-06-04
EARLIER FILING DATE: 1996-06-05
SOFTWARE: PALCATION NUMBER: AU PO 0265
SARLIER APPLICATION NUMBER: AU PO 0265
SARLIER APPLICATION NUMBER: AU PO 0265
SOFTWARE: PALCH OF VET. 2.1
SEQ ID NOS: 44
SOFTWARE: PALCH OF VET. 2.1
                                                      TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of TITLE OF INVENTION: Respiratory Syncytial Virus FILE REFERENCE: 415852001010 Syncytial Virus CURRENT APPLICATION NUMBER: US/09/202,035 CURRENT PILING DATE: 1998-12-17 EARLIER PILING DATE: 1997-06-04 EARLIER PILING DATE: 1997-06-04 EARLIER PILING DATE: 1997-06-05 NUMBER: PLOTOR NUMBER: AU PO 0265 EARLIER FILING DATE: 1996-06-05 NUMBER PILING DATE: 1996-06-05 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-202-035-5
; Sequence 5, Application US/09202035
; SERERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Respiratory Syncytial Virus
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
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Pred. No. 2.3e-25;
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CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PCI/AU97/00351
EARLIER FILING DATE: 1997-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: respiratory syncytial virus US-09-202-035-3
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                  Sequence 2, Application US/09202035 GENERAL INFORMATION:
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98.0%;
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Best Local Similarity
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Matches 48; Conserv
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US-09-202-035-3
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LENGTH: 49
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US-60-208-701-2
US-60-208-701-2
Sequence 2, Application US/60208701
Sequence 2. Application US/60208701
September INFORMATION:
APPLICANT: Portner, Allen
APPLICANT: TAIRMOO, TOTU
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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                         1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
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NAME/KEY: SITE
LOCATION: (1)
FEATURE:
NAME/KEY: SITE
NAME/KEY: SITE
NAME/KEY: SITE
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100.0%; Pred. No. 6.1e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                              APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural
TITLE OF INVENTION: Wiral Peptides with Structural
FITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415822000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PQT/AU97/00351
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 43
LENGTH: 49
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CURRENT APPLICATION NOWBER: US/60/208,701
CURRENT FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: respiratory syncytial virus
                                                                                                                                              US-09-202-035-43; Sequence 43, Application US/09202035; GENERAL INFORMATION:
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; OTHER INFORMATION: amidation
US-09-202-035-43
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Best Local Similarity 100.0 Matches 49; Conservative
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LENGTH: 298
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APPLICATE: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REPERBUCE: 41585200100
CURRENT FILIGE DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1996-06-05
WUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
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Sequence 40, Application US/09647309A

Sequence 40, Application US/09647309A

GENERAL INFORMATION:

TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY

FILE REPRENCE: D17064

CURRENT APPLICATION NUMBER: US/09/647,309A

CURRENT FILING DATE: 1998-03-28

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 136

SOFTWARE: Patentin Vers. 2.0

SEQ ID NO 40
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GENERAL INFORMATION:
APPLICANT: Pierre Febre Medicament
TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
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Local Similarity 98.0%; Score 285; DB 20; Length 59
Local Similarity 98.0%; Pred. No. 2.8e-25;
es 48; Conservative 1; Mismatches 0; Indels
1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                              1 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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                                        Indels
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Pred. No. 2.3e-25;
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Pred. No. 2.3e-25;
           98.0%; Pred. ....+ive 1; Mismatches
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ORGANISM: Respiratory syncytial Virus (RSV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: respiratory syncytial virus US-09-202-035-8
                                                                                                                                                                                                                                                 Sequence 8, Application US/09202035 GENERAL INFORMATION:
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98.0%;
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Best Local Similarity 98.0 Matches 48; Conservative
                     Best Local Similarity 98.0
Matches 48; Conservative
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Best Local Similarity
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US-09-647-309A-38
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US-09-202-035-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
TATULE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFRENCE: 418852000100
CURRENT PRILING DATE: 1998-12-17
EARLIER PEPLICATION NUMBER: PCT/AU97/00351
EARLIER PELING DATE: 19997-06-04
EARLIER PELING DATE: 1996-06-05
EARLIER PILING DATE: 1996-06-05
SOUTHWARE: PATENTION NUMBER: AV
SOFTWARE: PATENTIN VET. 2.1
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE REFRENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER PAPLICATION NUMBER: POT/A097/00351
EARLIER PILING DATE: 1997-06-04
ERRIER PILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 2.3e-25;
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Pred. No. 2.3e-25;
                                                                                                                                                                                                                                                                                               1; Mismatches
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              EARLIER APPLICATION NUMBER: AU PO 0265
BARLIER FILING DATE: 1996-06-05
NUMBER OF SEC ID NOS: 44
SOFTWARE: PETENTIN VET. 2.1
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Matches 48; Conserv
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US-09-202-035-6
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US-09-202-035-7
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                                                                                                         SEQ ID NO 5
LENGTH: 49
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Gaps

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Length 49;

DB 16;

Score 285;

90.66

Query Match

Search completed: November 22, 2002, 14:29:48 Job time : 142 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 22, 2002, 14:24:42; Search time 18 Seconds Run on:

(without alignments) 261.699 Million cell updates/sec

US-09-202-035-1 288 1 KQRQNKPPSKPNNDFHFEVF......NNPTCWAICKIPNKKPGKK Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	major surface qlyc			attachment protein	major surface glyc	G protein - Human	attachment protein	attachment protein	attachment protein	major surface glyc	surface	ø	protein G	glycoprotein G - b	glycoprotein G - b	glycoprotein G - o	attachment glycopr	diaminopimelate ep		diaminopimelate ep			charybdotoxin 2 -	diaminopimelate ep		charybdotoxin 1 [v	diaminopimelate ep	สา	hypothetical prote
SUMMARIES	£	MGNZ	JQ1205	-	-	_	JC5680			-	MGNZ18	MGNZ60								-			F86067						AD3432	Æ
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Accession: J01205
attachment protein - human respiratory syncytial virus (strain RSB1734)
wild-205
attachment protein - human respiratory syncytial virus
c; pecies: human respiratory syncytial virus
c; Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997
c; Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997
c; Accession: J01208
R; Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A; Fitle: Identification of variable domains of the attachment (G) protein of subgroup A; Reference number: J01204; MUID: 91374005; PMID: 1895054
A; Molecule type: mRNA

RESULT 2

neurotoxin Ts-kapp	diaminopimelate ep	diaminopimelate ep	hypothetical prote	probable protein k	diaminopimelate ep	probable E2F5 fami	hypothetical prote	gene el protein -	hypothetical prote	basic juvenile hor	T-cell surface gly	sex-specific stora	hypothetical prote	SYG1 protein - yea	signal peptidase I
S70473	G82986	T10459	T25507	T02584	C70458	G84775	A71822	S48861	T08663	B45046	150610	S01918	E82713	S49931	B84947
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57	276	276	518	116	279	532	792	1188	117	748	235	747	266	902	160
20.5	20.3	20.0	20.0	20.0	19.8	19.8	19.8	19.8	19.6	19.6	19.3	19.3	19.1	18.9	18.8
59	58.5	57.5	57.5	57.5	57	57	57	57	56.5	56.5	55.5	55.5	55	54.5	54
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

MGNZ  major surface glycoprotein G - human respiratory syncytial virus C; Species: human respiratory syncytial virus C; Species: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999 C; Accession: A94048, A93599; A04039 R; Wertz, G.W., ; Collins, P-ExHugang,—X.,; Gruber, C.; Levine, S.; Ball, L.A. Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985 A; Title: Nucleotide sequence of the G protein gene of human respiratory syncytial vir A; Reference number: A94048; MUD:85216636; PMID:3858865 A; Reference number: MA94048 A; Rolecule type: MRNA	ratory syncytial virus us ws ws ws ws ws ws cs
A; Rosidues: 1.298 (WER> A; Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; A; Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; A; Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid prott A; Note: this protein may carry 40-80 separate O-linked carbohydrate chains distribute R; Satake, M; Coligan, J.E., Elango, N; Norrby, E.; Venkatesan, S. Nucleic Acids Res. 13, 7795-7812, 1985 A; Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.	GB:KO2719; GB:KO3348; GB:KO3349; GB:M11217; h residues 376-467 of the nucleocapsid prot ate O-linked carbohydrate chains distribute orrby, E.; Venkatesan, S. ope 91ycoprotein (G) has a novel structure. PMID:4069997
A; Molecule type: MRNA A; Residues: 1-298 <sat> A; Residues: 1-298 <sat> A; Cross_references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998 A; Cross_references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998 C; Superfamily: respiratory syncytial virus major surface glycoprotein G C; Keywords: glycoprotein; transmembrane protein F; 38-66/Domain: transmembrane #status predicted <tnm> F; 38-56/Domain: transmembrane #status predicted <anm> F; 85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted</anm></tnm></sat></sat>	PIDN:CAA26928.1; PID:g60998 major surface glycoprotein G otein icted <tnm> e (Asn) (covalent) #status predicted</tnm>
Query Match 100.0%; Score 288; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 1.7e-26; Matches 49; Conservative 0; Mismatches 0; Indels Qy .1 KORONKPPSKPNNDFHEVFNFVPGSICSNNPTGMAICKRIPNKKPGKK 49	88; DB 1; Length 298; o. 1.7e-26; tches, 0; Indels 0; Gaps 0;

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UC5680
G protein - Human respiratory syncytial virus
C; Species: Human respiratory syncytial virus
C; Species: Human respiratory syncytial virus
C; Species: Human respiratory syncytial virus
C; Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 26-Feb-1998
C; Accession: JC5680
R; Gend, X: Wang, Z: Qian, Y: Zhu, R: Deng, J: Du, J.; Zhu, Z.
Chinese J. Virol. 12, 317-322, 1996
A; Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain
A; Reference number: JC5680
A; Accession: JC5680
A; Molecula type: mRNA
A; Residues: 1-298 <GEN>
A; Residues: 1-298 <GEN>
A; Residues: 1-298 <GEN>
A; Roperimental source: strain B79
A; Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for C; Superfamily: respiratory syncytial virus major surface glycoprotein G
E; 1-38/Domain: intracellular #status predicted <INM>
F; 9-66/Domain: transmembrane #status predicted <INM>
F; 9-66/Domain: cransmembrane #status predicted <INMP
F; 9-66/Domain: cransmembrane #status pred
                                                                                                                                     C; Species: human respiratory syncytial virus
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C; Accession: A32703; S12279
E; Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A; Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A; Reference number: A32703; MUID:87289657; PMID:2441388
                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A32703
A;Molecule type: mRNA
A;Rosidues: 1-298 «JOH»
A;Cross-references: GB:M17212; NID:g333940; PIDN:AAA47411.1; PID:g333941
A;Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
EMBO J. 9, 4181-4187, 1990
A;Title: Frame shift mutations as a novel mechanism for the generation of neutraliza.
A;Reference number: S12279; MUID:91065351; PMID:2249671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule Lype: Marka
A; Residues: 1-298 «GAR»
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Keywords: glycoprotein; transmembrane protein
F; 41-63/Domain: transmembrane #status predicted <TMN>
F; 85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #st-
                                                                                                              respiratory syncytial virus (strain Long)
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N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: J01207
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
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3.9e-26;
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                                                                                                                  G - human
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F:85,103,135,237,251,273,294/Blnding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                           predicted
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J. Gen. Virol. 72, 2001-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup
A;Reference number: JQ1204; MUID:91374005; PMID:1895054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JQ1204
A; Molecule type: mRNA
A; Residues: 1-297 <CAN>
C; Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ildren and adults.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2001-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A;Reference number: JQ1204; MUID:91374005; PMID:1895054
A;Accession: JQ1208
                                      Respiratory syncytial virus commonly causes severe lower respiratory tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tract
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A;Residues: 1-597 <CAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory
ildren and adults.
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                                                             ildren and adults.
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attachment protein - human respiratory syncytial virus (strain RSB642)
N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1204
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1208
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                                                                                                                                                                                                                                                        Score 285; DB 2; Length 297;
Pred. No. 3.9e-26;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               149 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKR 197
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Pred. No. 3.9e-26;
1; Mismatches 0; Indels
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Pred. No. 3.9e-26;
1; Mismatches 0; Indels
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98.0%;
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Local Similarity 98.0%;
les 48; Conservative
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98.0%;
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Best Local Similarity
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A; Residues: 1-297
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Matches
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C;Accession: B32703
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388
A;Accession: B32703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N.Alternate names: attachment glycoprotein G
C;Species: human respiratory syncytial virus
C;Deteis: human respiratory syncytial virus
C;Dete: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A37077
R;Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A;Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis gous subgroup virus challenge.
A;Reference number: A37077; MUID:90357765; PMID:1697126
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S;Reywords: glycoprotein; transmembrane protein
F;45-63/Domain: transmembrane #status predicted <TMN>
F;81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major surface glycoprotein G - bovine respiratory syncytial virus (strain 391-2) N. Alternate names: attachment glycoprotein G C. Species: bovine respiratory syncytial virus C. Species: bovine respiratory syncytial virus C. Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                               major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA

A; Residues: 1-292 <.OGH.

A; Cross-references: GB:M/7213; NID:g333942; PIDN:AAA47412.1; PID:g333943

C; Superfamily: respiratory syncytial virus major surface glycoprotein G

C; Superfamily: respiratory syncytial virus major surface glycoprotein G

C; Superfamily: respiratory syncytial virus major surface glycoprotein G

C; Keywords: glycoprotein; transmembrane #status predicted <TMN>

F; 81.63/Domain: transmembrane #status predicted <TMN>

F; 81, 86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 5.7e-15;
4; Mismatches 13; Indels
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                                                                             149 KSRSKNPPKRPKDDYHFEVPRFYPCSICGNNQLCKSICKTIPSNKPKKK 197
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                 2; Indels
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Pred. No. 5.7e-15;
4; Mismatches 13;
                 Mismatches
                 Ξ,
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Best Local Similarity 65.3%;
Matches 32; Conservative
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1larity 65.3%;
Conservative
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Best Local Similarity
Matches 32; Conserv
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A; Molecule type: mRNA
A; Residues: 1-292 <SUL>
                 46;
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MGNZ60
                 Matches
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N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: J01209
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A
A;Reference number: J01204; MUID:91374005; PMID:1895054
A;Reference number: J01204; MUID:91374005; PMID:1895054
A;Residues: 1-297 ccAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
C;Comment: Respiratory syncytial virus major surface glycoprotein G
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Reywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
J. Gen. Virol. 72, 2091-2096, 1991
A) Title: Identification of variable domains of the attachment (G) protein of subgroup A A) Reference number: J01204; MUID: 91374005; PMID: 1895054
A) Accession: J01207
A) Molecule type: mRNA
A) Residues: 1-298 cCAN>
A) Residues: 1-298 cCAN>
A) Note: the authors translated the codon ACC for residue 4 as Asn and AGC for residue 22 C; Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ill didren and adults.
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Keywords: glycoprotein; transmembrane protein
F; 85, 103, 135, 237, 250, 273, 294/Binding site: carbohydrate (Asn) (covalent) #status predict
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N.Alternate names: G protein
C.Species: human respiratory syncytial virus
C.Species: human respiratory syncytial virus
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C.Accession: J01206
N.Canc. P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A.Title: Identification of variable domains of the attachment (G) protein of subgroup A; Reference number: J01204; MUID:91374005; PMID:1895054
A.Accession: J01206
A.Molecule type: mRNA
A.Residues: 1-297 ccAN>
C.Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ildren and adults.
C.Scomment: Respiratory syncytial virus major surface glycoprotein G
C; Keywords: glycoprotein; transmembrane protein
F; 85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predi
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Pred. No. 2e-25;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 298,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 97.2%; Score 280; DB 2; Le Local Similarity 95.9%; Pred. No. 1.5e-25; les 47; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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Pred. No. 1e-24;
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93.9%;
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ilarity 95.9%;
Conservative
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                           RiLerch, R.A.; Anderson, K.; Wertz, G.W.
J. Virol. 64, 5559-5569, 1990
A;Title: Nucleotide sequence analysis and expression from recombinant vectors demonstrat
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J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial
A;Reference number: JQ2284; MUID:93389461; PMID:8376974
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C;Sate: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: P00768
R;Mallipeddi, S.K.; Samal, S.K.
J; Genl, Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial
A;Reference number: JQ2284; MUID:93389461; PMID:8376974
                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;45-62/Domain: transmembrane #status predicted <TMN>
F;3,85,127,149,233,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Superfamily: respiratory syncytial virus major surface glycoprotein G
C.Supyords: glycoprotein; transmembrane protein
F.1-38/Domain: intransmembrane #status predicted ACYT>
F.39-66/Domain: transmembrane #status predicted FEXT>
F.67-263/Domain: extraocallular #status predicted <br/>FEXT>
F.127,163,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: bovine respiratory syncytial virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: JQ2284
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C Superfamily: respiratory syncytial virus major surface glycoprotein G C; Superfamily: respiratory syncytial virus major surface glycoprotein G C; Keywords: glycoprotein; transmembrane protein F:1-31/Domain: intracellular #status predicted <IMT>
F:32-59/Domain: transmembrane #status predicted <IMM>
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29.6%; Pred. No. 0.017;
.ive 9; Mismatches 16; Indels
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Pred. No. 0.044;
9; Mismatches 20; Indels
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                                                                                                                            y syncytial virus.
A;Reference number: A36408; MUID:91012801; PMID:2214024
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Local Similarity 29.8%;
hes 14; Conservative
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hes 16; Conservative
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A; Residues: 1-257 <LER>
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A; Residues: 1-250 <MAL>
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C; Accession: A36408
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C. Accession: P00769
R.Mallipeddi, S.K.; Samal, S.K.
J. General topology of the glycoprotein gene of bovine respiratory syncytial of the second of the glycoprotein gene of bovine respiratory syncytial statemence number: J02284; MUID: 93389461; PMID: 8376974
A. Reference number: J02284; MUID: 93389461; PMID: 8376974
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-248 cMAL>
B. 30-57/Domain: transmembrane #status predicted cMAN>
F. 30-57/Domain: extracellular #status predicted cEXT>
F;60-250/Domain: extracellular #status predicted <EXT>
F;78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: bovine respiratory syncytial virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
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                                                                                                                                                                Query Match 27.4%; Score 79; DB 2; Length 250; Best Local Similarity 26.7%; Pred. No. 0.055; Matches 12; Conservative 11; Mismatches 22; Indels
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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 22, 2002, 14:17:16 ; Search time 11 Seconds (without alignments) 184.758 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-202-035-1 288 1 KQRQNKPPSKPNNDFHFEVP......NNPTCWAICKRIPNKKPGKK 49

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query	y h Length	DB	ID	Description
п		100	0 29	Т		P03423 human respi
61	285	O)		7	VGLG_HRSV2	1 human
Э	285	99.0	53	П	VGLG_HRSV3	human
4	285	σ	. 29	П	VGLG_HRSV6	P27025 human respi
ഗ	285	Q)	29	1	VGLG_HRSVL	human
9	280	97	29	Н	VGLG_HRSV5	human
7	279	96.9	9 297	Н	VGLG_HRSV4	human
80	273	94	29	-	VGLG_HRSV7	human
6	190	.99	29	Н	VGLG_HRSV1	human
10	190	99	29	<b>,</b> →	VGLG_HRSV8	human
11	83.5	29.	25	Н	VGLG_BRSVC	bovine
12	80	27.	26	-	VGLG_BRSV2	bovine
13	77.5	26.9	25	~	VGLG_BRSVS	bovine
14	77.5	76.	26	-	VGLG_BRSVW	bovine
15	77.5	76	56	~	VGLG_ORSVW	ovine r
16	76.5	76.	26	٦	VGLG_BRSV1	bovine
17		26.6	26	~	VGLG_BRSV4	bovine
18	74	25.	25	-	VGLG_BRSVL	bovine
19	74	25.7	25	1	VGLG_BRSVR	bovine
20	73	25.3		~	VGLG_BRSV7	Q65706 bovine resp
21	67.5	23.	.4 274	_	DAPF_PASMU	pasteur
22		23		1	DAPF_ECO57	Q8x8p8 escherichia
23		23.1	27	-	DAPF_ECOLI	P08885 escherichia
24		23.	27	-	DAPF_SALTY	Q916p6 salmonella
25	66.5	m	27	7	DAPF_YERPE	P46357 yersinia pe
56		CV.	2 37	-	SCK2_LEIQH	
27	63.5		27	Н	DAPF_HAEIN	P44859 haemophilus
28	62	ij	5 37	-		7 leturus
29	62	Н	~		DAPF_VIBCH	Q9kv16 vibrio chol
30	60.5	ä	2	Н	SCK1_MESMA	Q9nii6 mesobuthus
31	58.5	٠	27	П		
32	57.5	20.	0 276	Н		322
33	57	٠		П	DAPF_AQUAE	067693 aquifex aeo

Q06342 trichoplusi P09179 bombyx mori	P56219 tityus serr Q9nii5 mesobuthus P40528 saccharomyc	Q9kivl haemophilus P57248 buchnera ap	P97436 mus musculu P57649 buchnera ap	P34878 lactococcus P11332 european el	
JSB1_TRINI SSP1_BOMMO	SCKZ_MESMA SCK2_MESMA SYG1_YEAST	HGBB_HAEIN LSPA_BUCAI	HK31_MOUSE DAPF_BUCAI	MTSB_LACLC VE7_PAPVE	TR1A_MOUSE
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748	35 58 902	1067	237	360 102	454
19.6 19.3	19.1 18.9 18.9	18.9 18.8	18.6	18.2 18.1	18.1
56.5	54.5 54.5	54.5 54	53.5	52.5 52	52
34 35	36 37 38	39 40	41	4 4 4	45

# ALIGNMENTS

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NCBI_TaxID=11253;
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A MEDLINE=91374005; PubMed=1895054;

A Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Tidentification of variable domains of the attachment (G) protein of variable domains of v
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                (See http://www.isb-sib.ch/announce/
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

993C3D2DD68BC634 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.0%; Score 285; DB 1; Length 297; 98.0%; Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human respiratory syncytial virus (strain rsb642).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11252;
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   Usage by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FC72A7F3A8EBF67C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 288; DB 1; 100.0%; Pred. No. 6.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
dified and this statement is not removed. Lities requires a license agreement (See Psend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                            EMBL; uosca.,
PIR; A04039; MGNZ.
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                         32586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32745 MW;
                                                                  EMBL; M11486; AAB59857.1; -. EMBL; X03149; CAA26928.1; -. EMBL; U50362; AAB86663.1; -. EMBL; U50363; AAB86675.1; -. EMBL; U63644; AAC55969.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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135
144
144
237
297 AA;
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 modified and
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P27021;
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DOMAIN
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CARBOHYD
              entities
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CARBOHYD
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MEDLINE-91374005; PubMed=1895054;
MEDLINE-91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
I. Gen. Virol. 72:2091-2096(1991).
RESPIRATORY SYNCYTIAL YIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
I- SUBCELLUAR LOCATION: EXPERSSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CELLS AND INCORPORATE COLINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                      149 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKR 197
KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPICWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA nėgativė-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11256;
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                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48448F9E091E1802 CRC64;
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                                                                                                                                                                                                                                                                                                          Human respiratory syncytial virus (strain rsb1734)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human respiratory syncytial virus (strain rsb6256)
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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98.0%; Pred. No. 1...
1; Mismatches
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InterPro; PR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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135 N-
237 N-
251 N-
32525 MW;
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                                                                                                                                                        STANDARD;
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135 1
237 2
251 2
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Best Local Similarity
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VGLG_HRSV4
P27023;
  TRANSMEM
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VGLG_HRSV5
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VGLG_HRSV4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-8730957; PubMed=2441388;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
The G glycoprotein of human respiratory syncytial viruses of
subgroups A and B: extensive sequence divergence between
antigenically related proteins.;
Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
PRESPIRATOR: UNLIKE THE OPHERR PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                                       Gaps
                                     -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
PIR; JQ1208; JRP000925; Glycoprot_G.
Pfam: PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRARM OF THE VIRIONS.
-1- PTM: MAY CARRY 40-460 SEPRARTE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
6781756C38B64A80 CRC64;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11260;
                                                                                                                                                                                                                                                                                          Length 297;
                                                                                                                                                                                                                                                                                                                                                             149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                               1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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Pred. No. 1.5e-26;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
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InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                        99.0%;
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103
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294
297 AA;
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ses 48; Conserv
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P20895;
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CARBOHYD
SEQUENCE
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CARBOHYD
                                                                                                                                                                 TRANSMEM
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J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL, VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
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-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
            EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11255;
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                                                                                                                                      B79FEFA4B4A73B0E CRC64;
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                                                                                                                                                                          1.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human respiratory syncytial virus (strain rsb6190)
                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 39, Last annotation update)
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1; Mismatches
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                                                                                                                                                                       Score 285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
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MEDLINE=91374005; Pubmed=1895054;
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InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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                                                                              Transmembrane; Glycoprotein.
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nes 46; Conserv
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                                                                                                                                                                                                                                               subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).

J. Gen. Virol. 72:2091-2096(1991).

HEMAGGIUTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURANINIDASE AND HEMAGGIUTINATING ACTIVITIES.

J. SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

JISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

PIR; JO1206, JO1206.

JO1206, JO1206, JO1206.

FYAND STRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

PIR; JO1206, JO1206.

PÉRM: PROVO802; Glycoprotein.

Transmembrane; Glycoprotein.
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[Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";

[Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";

[Iden. Virol. 72:2091-2096(1991).

[Iden. Virol. 72:2091].

[Iden. Virol
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                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-91374005; PubMed-1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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-has 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus (strain rsb6614).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                         Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                        Human respiratory syncytial virus (strain rsb5857)
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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1; Mismatches
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Local Similarity 95.9%;
Les 47; Conservative
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P27026;
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"The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigenically related proteins.";

Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).

-!- FONCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL, VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
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-i- PTM: MAY CARRY 40-40 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREOMINE RESIDUES.
                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
58B384028E437ACD CRC64;
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

BC8C59F69CA7AFC2 CRC64;
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Viruses; saRNA negative-strand viruses; Mononegavirales;
ParamyxovIridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID-11251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.8%; Score 273; DB 1; Length 297; ilarity 93.9%; Pred. No. 4e-25; Conservative 1; Mismatches 2; Indels
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01-NOV-1991 (Rel. 20, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
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PIR; JQ1209; JQ1209.
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;
"Genetic diversity of the attachment protein of subgroup B
respiratory syncytial viruses.";
J. Virol. 65:5425-5434(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAWXXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sullender W.M., Anderson K., Wertz G.W.;
"The respiratory syncytial virus subgroup B attachment glycoprotein:
analysis of sequence, expression from a recombinant vector, and
evaluation as an immunogen against homologous and heterologous
subgroup virus challenge.";
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-1- PTM: MAY CARRY 40-96 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus (subgroup B / strain 8/60). Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
   Length 292;
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                                                                                         149 KSRSKNPPKKPKDDYHFEVFNFVPCSICGNNQLCKSICKTIPSNKPKKK 197
                                                                      1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                     13; Indels
                                                                                                                                                                                                                                                                                         Major surface glycoprotein G (Attachment glycoprotein G)
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Pred. No. 2.2e-15;
4; Mismatches 13;
 Score 190; DB 1;
Pred. No. 2.2e-15;
4; Mismatches 13
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-91374595; Pubmed-1895391;
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Pfam; PF00802; Glycoprotein_G; I.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
01-AUG-1992 (Rel. 23, Last anno
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292 E3
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32143 MW;
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65.3%;
 65.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subgroup virus challenge.";
Virology 178:195-203(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M55633; AAA47413.1;
Query Match
Best Local Similarity 65.3
Matches 32; Conservative
                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                               VGLG_HRSV8
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TRANSMEM
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Gaps

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Indels

13;

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32;

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Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine respiratory syncytial virus.";
Biochemistry 35:14664-14668(1996).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=91012801; PubMed=2214024;
Lerch R.A., Anderson K., Wertz G.W.;
Lerch R.A., Anderson analysis and expression from recombinant vectors demonstrate that the attachment protein G of bovine respiratory syncytial virus is distinct from that of human respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                 Bovine respiratory syncytial virus (strain Copenhagen) (BRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97098087; PubMed=8942628;
DoreLeijers J.F., Langedijk J.P.M., Haard K., Boelens R.,
Rullmann J.A., Schaaper W.M., van Oirschot J.T., Kapteln R.;
"Solution structure of the immunodominant region of protein (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.5; DB 1; Length 257;
Pred. No. 0.0063;
9; Mismatches 16; Indels 13
                Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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POTENTIAL.
EXTRACELLULAR (POTENTIAL).
1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
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                                                                                                                                                                      Last annotation update)
                                                                                                                                                      Last sequence update)
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PDB; 1BRV; 05-JUN-97.
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein; 3D-structure.
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29.6%;
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01-AUG-1991 (Rel. 19,
15-JUL-1998 (Rel. 36,
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257 AA;
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es 16; Conserv
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                                                                                                                                                                                                                                                                                        RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=9728834; PubMed-9143302;
MEDLINE=7788834; S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
                                                                                                                                                                                                                                                      degree of genetic homogeneity.";
Virology 231:48-58(1997).
1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
             6 KPPSKPNNDF-----HFEVFNFVPCSICSNNPTCWAIC----KRIPNKKP 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%; Score 80; DB 1; Length 263; 29.8%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                 Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                     Bovine respiratory syncytial virus (strain 220-60) (BRS) VIRUSES; SSRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus. NCBL_TaxID=82819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                              [5-JUL_1998 (Rel. 36, Created)
[5-JUL-1998 (Rel. 36, Last sequence update)
[5-JUL-1998 (Rel. 36, Last annotation update)
                                                                            263 AA.
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BY SIMILARITY.
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73 186
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127
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163 1
28964 MW;
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263 AA;
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                                                                                                                                                                                                                                                                             degree of genetic homogeneity.";
Virology 231:48-58(1997).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNOYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97288324; PubMed-9143302;
MEDLINE 57.888324; PubMed-9143302;
"Antigenically distinct G glycoproteins of BRSV strains share a high
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Furze J., Roberts S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
Virology 231:48-58(1997).
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-1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
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N-LINKED (GLONG...) (POTENTIAL).

N-LINKED (GLONG...) (POTENTIAL).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
Bovine respiratory syncytial virus (strain Snook) (BRS).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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257 AA;
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KPPSKP-----NNDFH--FEVFNFVPCSICSNNPTCWAIC------KR 40
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                                                                SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
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N-LINKED GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 77.5; DB 1; Length 263; 29.0%; Pred. No. 0.033; 1ve 5; Mismatches 19; Indels 2
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
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EXTRACELLULAR (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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InterPro.; PR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
                                        HEMAGGLUTINATING ACTIVITIES
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Matches 20; Conservative
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263 AA;
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the European He Swiss Institute of Bloinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.

EXTRACELLULAR (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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10; Mismatches 18; Indels 2:
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Job time : 12 secs
                                                                                                                                                                                                                                                        Interpro; IPR000925; Glycoprot_G. Pfam; PF00802; Glycoprotein_G; 1. Transmembrane; Glycoprotein.
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EMBL; S67862; AAB29551.1; JOINED.
HSSP; P22261; 1BRV.
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Matches 17; Conservative
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"Antigenic and genetic diversity among the attachment proteins of group A respiratory syncytial viruses that have caused repeat infections in children.";
J. Infect. Dis. 178:925-932(1998).
EMBL, AF065407; AAD02943.1;
InterPro: IPR000386; Flycoprot.G.
InterPro: IPR000386; Pantin-attach.
InterPro: IPR002956; P. rich—extensn.
Pfam: PF000802; Glycoprotein.G: 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Attachment glycoprotein G (Fragment)
Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 288; DB 12;
.larity 100.0%; Pred. No. 1.6e-31;
Conservative 0; Mismatches 0;
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Q9Q6S8
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Q9YVB0
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MEDLINE=99022964; PubMed=9806017;
PRELIMINARY;
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subgroups A and B of respiratory syncytial virus isolated over sonsecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
EMBL, AF193312; AAF23735.1;
EnterPro; IPR000925; Glycoprot_G.
InterPro; IPR003808; Papathe_attach.
InterPro; IPR002965; P_rich_extensn.
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   Length 278;
                                                                                               130 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 178
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                                         Indels
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Viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Viruses; SRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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PRINTS; PR01217; PRICHEXTENSN.
PROSITS; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 Score 285; DB 12;
Pred. No. 3.8e-31;
1; Mismatches 0;
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01-MAR-2002 (TrEMBLrel. 20, Last anno
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01-MAR-2002 (TrEMBLrel. 20, Last ann
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MEDLINE=20283719; PubMed=10823752;
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 99.0%;
Query Match
Best Local Similarity 98.0
Matches 48; Conservative
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"Genetic diversity and molecular epidemiology of the g protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

MRL; AF193309; AF123732.1;

InterPro; IPR000925; Glycoprot.G.

InterPro; IPR003880; Pantue_attach.

InterPro; IPR003880; Pantue_attach.

InterPro; IPR003880; Pantue_attach.

PRINTS; PR01217; PRICHETENSN.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                     Choi E.H., Lee H.J.;

Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11250;
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                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 285; DB 12;
Pred. No. 3.8e-31;
1; Mismatches 0;
                                       278 AA
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                                                                                                                                                                                                                                                                                                                                                                                   consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
RMBL, AF193305; AAF23728.1;
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR003880; Ppantne_attach.
InterPro; IPR003880; Prich_extensn.
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                                         PRT;
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                                                                                                                                                                           Human respiratory syncytial virus.
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MEDLINE-20283719; PubMed=10823752;
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1 Similarity 98.0%;
48; Conservative
                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
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                                       PRELIMINARY;
                                                                                                                                     Glycoprotein (Fragment).
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Length 279;

Score 285; DB 12; Pred. No. 3.8e-31;

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Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein a subgroups A and B of respiratory syncytial virus isolated over consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193306; AAF23729.1;
InterPro; IPR000925; Glycoprot.G.
InterPro; IPR000802; Glycoprotein.G.
FROM: PF00802; Glycoprotein.G.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN.I.
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98.0%; Pred. No. 3.c.
... 1; Mismatches
                                                             STRAIN=91242;
MEDLINE=20283719; PubMed=10823752;
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Best Local Similarity 98.0°
Matches 48; Conservative
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Q9Q6T9
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Q9Q6T8
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C STRAIN=94191;
MEDLINE=20283191;
MEDLINE=20283191;
MEDLINE=20283191;
MEDLINE=20283191;
MEDLINE=20283191;
MEDLINE=20283191;
MIGHAL SA And B of respiratory syncytial virus isolated over 9 subgroups A and B of respiratory syncytial virus isolated over 9 tonsecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
R. MILEPPO: IPR000925; G19coprot.G.
R. InterPro: IPR000925; G19coprot.G.
R. InterPro: IPR0009265; P10ch.extensn.
R. PF00802; G19coprotin.G.
R. PRINTS: PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                             Length 278;
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98.0%; Pred. No. 3.8e-31;
iive 1; Mismatches 0; Indels
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Last annotation update)
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                                                                                    InterPro; IPR002965; P_rich_extensn.
Pfam; PF00802; Glycoprotein_G; 1.
PRIWRS; PROLIT7; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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                             InterPro; IPR000925; Glycoprot_G.
InterPro; IPR003880; Ppantne_attach.
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EMBL; AF193313; AAF23736.1; -
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Best Local Similarity
Matches 48; Conserv
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01-MAR-2002
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"Genetic diversity and molecular epidemiology of the G protein a subgroups A and B of respiratory syncytial virus isolated over sonsecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
BMBL; AF193307; AAF23730.1;
InterPro: IPR000925; Glycoprot_G.
InterPro: IPR000986; Ppantne_attach.
InterPro: IPR0002965; P_rich_extensn.
Prim; PR00802; Glycoprot_G.
InterPro: IPR0002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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130 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKK 178
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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98.0%; Pred. No. 3.8e-31;
ive 1; Mismatches 0;
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MEDLINE=20283719; PubMed=10823752;
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Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193314; AAF23737.1;
InterPro; IPR000325; Glycoprot.G.
InterPro; IPR003880; Ppantne_attach.
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BDLINR-20283719; PubMed-10823752;
Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Pred. No. 3.8e-31;
1; Mismatches 0;
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Pfam; PF00802; Glycoprotein_G; 1.
PRIMES; PRO1217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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Pfam; PF00802; Glycoprotein_G; 1.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
NON_TER 1 1 1 SEQUENCE 279 AA; 30529 MW; AEC4D787983D472D
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J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193317; AAF23740.1; -.
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Interpro; IPR003880; Ppantne_attach.
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Best Local Similarity 98.0%;
Matches 48; Conservative
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01-MAR-2002
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Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

EMBL, AF19311; AAF23734.1;

InterPro: IPR000925; Glycoprot.G.

interPro: IPR003980; Pantne_attach.

InterPro: IPR003960; Pantne_attach.

InterPro: IPR003965; P.Lich.extensn.
                                                                                                                                                                                         choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
Brant. APR193308, APR29731.1;
InterPro; IPR003880; Papantne_attach.
Pfam; PF00802; Glycoprotein_G; 1.
Pfam; PF00802; Glycoprotein_G; 1.
Prosite, PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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                                                   Human respiratory syncytial virus.
Viruses; sRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
MCBI_TaxID=11250;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Last sequence update)
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Ol-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Pred. No. 3.8e-31;
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Pred. No. 3.8e-31;
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PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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MEDLINE=20283719; PubMed=10823752;
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                  Glycoprotein (Fragment)
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Score 285; DB 12; Pred. No. 3.8e-31; 1; Mismatches

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130 KQRQNKPPNKPNNDPHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 178
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                                               Pfan; PF00802; Glycoprotein_G; 1.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
          Interpro; IPR000925; Glycoprot_G.
Interpro; IPR003880; Ppantne_attach.
Interpro; IPR002965; P_rich_extensn.
EMBL; AF193320; AAF23743.1; -
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Best Local Similarity
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"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).

BMEL, AR19319; ARP23142.1;
InterPro; IPR00925; Glycoprot.G.
InterPro; IPR003880; Ppantne_attach.
InterPro; IPR002865; P_rich_extensn.
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            Score 285; DB 12; Length 279;
Pred. No. 3.8e-31;
1; Mismatches 0; Indels (
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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"Genetic diversity and molecular epidemiology of the G protein of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

EMBL, AR193326; AAR23749.1;

InterPro: IPR000325; Glycoprot.G.

InterPro: IPR000380; Painthe_attach.

InterPro: IPR002965; Prich_extensn.

PRINTS; PR01217; PRICHEXTENSN.

R PROSITE; PS00012; PROSPHOPANTETHEINE; UNKNOWN.1.

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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
                                                                                                                                                                                        Last sequence update)
Last annotation update)
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PRT;
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                                                                                                                    (TrEMBLrel. 13, CTrEMBLrel. 13, ICTEMBLrel. 13, ICTEMBLrel. 20, ICTEMBLrel. 20, ICTEMBLREL. 20, ICTEMBLREL. 20, ICTEMBLREL. 20, ICTEMBLREL. 20, ICTEMBLREL.
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PRELIMINARY;
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(without alignments)
69.765 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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                                  Compugen Ltd.
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compu
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# Result Query No. Score Match Length DB ID Description 1 56 21.5 37 10 US-10-044-359-28 Sequence 181, Appl 25 2 56 19.4 37 9 US-10-044-359-28 Sequence 20, Appl 26 3 54 18.8 57 9 US-10-044-359-18 Sequence 20, Appl 26 4 53 18.4 58 9 US-10-044-359-27 Sequence 20, Appl 27 5 117.7 325 9 US-10-044-359-18 Sequence 20, Appl 36 6 51 17.7 325 9 US-10-044-359-18 Sequence 11, Appl 36 7 51 17.7 325 9 US-10-044-359-11 Sequence 11, Appl 36 8 51 17.7 325 12 US-10-033-224-11 Sequence 11, Appl 36 10 51 17.7 325 12 US-10-033-224-11 Sequence 11, Appl 36 11 50.5 17.4 102 US-10-033-224-11<

Sequence 82, Appl Sequence 1151, Ap Sequence 14, Appl Sequence 11, Appl Sequence 11, Appl Sequence 10, Appl Sequence 6, Appl Sequence 6, Appl Sequence 15, Appl Sequence 14, Appl Sequence 24, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence	
0 US-09-726-643-82 0 US-09-925-300-1151 US-10-016-283-34 0 US-09-984-903-18 0 US-09-864-761-37986 0 US-09-864-761-37986 0 US-09-957-485-6 0 US-09-997-485-6 0 US-09-997-485-6 0 US-09-997-485-6 0 US-09-898-2215 US-09-898-2215 US-09-898-429-429 US-09-898-429-15 US-09-899-429-15 US-09-899-429-15 US-09-899-429-15 US-09-899-429-15 US-09-899-429-15 US-09-899-429-13 US-09-801-574-869-94 US-09-803-589-8 US-09-803-589-8 US-09-803-589-8 US-09-803-589-8 US-09-803-589-8 US-09-801-574-82 US-09-803-589-8 US-09-801-574-82 US-09-801-574-82 US-09-801-574-82	ALIGNMEN
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Sequence 181, Application US/09030619B

Sequence 181, Application US/09030619B

Patent No. US2002003561A1

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Taylor, Robert

APPLICANT: Frager, Janet R.

APPLICANT: Meat, Michael H.P.

APPLICANT: West, Michael H.P.

APPLICANT: West, Michael H.P.

APPLICANT: West, Michael H.P.

TITLE OF INVENTION: COMPOSITIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

TITLE OF INVENTION: WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 181

LENGTH: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/10044359; Patent No. US20020160454A1; GENERAL INFORMATION:
APPLICANT: Herrman, Rafael; APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CSNNPTCWAICKRIPNKKPGK 48
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JS-09-030-619-181
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US-10-044-359-28
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TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                     14 CSISIYSEADLIDVKCISSQECWIACKKVTGRFQGK 49
                                                                                                                                                                                                                                                     Score 53; DB 9
Pred. No. 3.6;
5; Mismatches
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Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: Herman, Rafael
APPLICANT: Hornwation:
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICTOSOft Office 97
SEQ ID NO 27
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                 PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION WUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Mcrosoft Office 97
SEQ ID NO 18
LENGTH: 58
  PRIOR APPLICATION NUMBER: 09/599,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10033245
Patent No. US20020160392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-044-359-27; Sequence 27, Application US/10044359; Patent No. US20020160454A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Leiurus quinquestriatus US-10-044-359-27
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                                                                                                                                                                                        ; ORGANISM: Hottentotta judaica US-10-044-359-18
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Best Local Similarity 27.8%;
Matches 10; Conservative
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Best Local Similarity 33.3%;
Matches 7; Conservative
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Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumas, Daniel
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Botstein, David
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                                                                                                                                                                      TYPE: PRT
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                      Score 56; DB 9; Length 37; Pred. No. 0.97;
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                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
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                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WONG, James F.
APPLICANT: WOO, James F.
TITLE OF INVENTION: SCORPION TOXINS
TITLE OF INVENTION: SCORPION TOXINS
TITLE OF INVENTION: SCORPION TOXINS
FILE REPERENCE: BB1367 US NA
CURRENT FILING DATE: 2002-01-11
PRIOR PPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR PPLICATION NUMBER: 60/140,227
PRIOR PRILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICROSOFT Office 97
SED ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/10044359
Patent No. US20020160454A1
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Hee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILLE OF INVENTION: SCORPION TOXINS
FILLE PEFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
          CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILIG DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR PILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR PLING DATE: 1999-06-22
PRIOR FILING DATE: 1999-06-22
NUMBER: OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : || || || 6 LITEVICSIMISTEAQFIDVKCTSXKECWPICK 38
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Sequence 20, Application US/10044359
Patent No. US20020160454A1
SENERAL INFORMATION:
APPLICANT: Herrman, Rafael
TITLE OF INVENTION: SCORPION TOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                         28 CSNNPTCWAICKRIPNKKPGK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                               18.8%;
33.3%;
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Hottentotta judaica
                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Buthus martensii
US-10-044-359-28
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Matches 11; Conservative
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US-10-044-359-18
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                                                                                                                                                                                                         SEQ ID NO 28
LENGTH: 37
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Gaps
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                                                                                                    Pan,James
Roy,Margaret Ann
Stewart,Timothy A.
                                                                                                                                                                          Watanabe, Colin K.
Wood, William I.
             Ferrara, Napoleone
                              Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Gurney, Austin L.
                                                                                                                                                           Tumas, Daniel
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US-10-033-223-11
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/10/033,245 CURRENT PELING DATE: 2001-12-27 PRIOR PAPLICATION NUMBER: 06/095,325 PRIOR PAPLICATION NUMBER: 06/095,325 PRIOR PELICATION NUMBER: 06/095,325 PRIOR PELICATION NUMBER: 06/113,511 PRIOR PELICATION NUMBER: 06/115,58 PRIOR PELICATION NUMBER: 06/115,58 PRIOR PELICATION NUMBER: 06/115,33 PRIOR PELICATION NUMBER: 06/119,341 PRIOR PELICATION NUMBER: 06/119,341 PRIOR PELICATION NUMBER: 06/110,341 PRIOR PELICATION NUMBER: 06/110,341 PRIOR PELICATION NUMBER: 06/110,341 PRIOR PELICATION NUMBER: 06/110,341 PRIOR PELICATION NUMBER: 06/110,362 PRIOR PELICATION NUMBER: 06/110,362 PRIOR PELICATION NUMBER: 06/110,362 PRIOR PELICATION NUMBER: 06/110,362 PRIOR PELICATION NUMBER: 06/10,392/2851 PRIOR PELICATION NUMBER: 06/10,392/2851 PRIOR PELICATION NUMBER: 06/10,392/2851 PRIOR PELICATION NUMBER: PCT/US99/1252 PRIOR PELICATION NUMBER: PCT/US99/2851 PRIOR PELICATION OF SEQ ID NOS: 38
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Patent No. US20020164646A1
GENERAL INFORMATION:
APPLICANT: BOSTOCH, David
APPLICANT: Desnoyers, Luc
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Best Local Similarity 50.0%;
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-033-245-11
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US-10-033-223-11
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Gaps

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FITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 38;
1; Mismatches 8; Indels
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CURRENT FALLING DATE: 2001-12-27

PRIOR PAPLICATION NUMBER: 60/095,325

PRIOR PELING DATE: 1998-08-04

PRIOR PELING DATE: 1998-12-16

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1999-01-12

PRIOR PILING DATE: 1999-01-12

PRIOR PELICATION NUMBER: 60/115,558

PRIOR PELICATION NUMBER: 60/115,558

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-02

PRIOR PELING DATE: 1999-01-02

PRIOR PELING DATE: 1999-02-09

PRIOR PELING DATE: 1999-02-09

PRIOR PELING DATE: 1999-02-09

PRIOR PELING DATE: 1999-02-10

PRIOR PELING DATE: 1999-02-10

PRIOR PELING DATE: 1999-02-10

PRIOR PELING DATE: 1999-02-10

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-03-3

PRIOR PELING DATE: 1999-06-03

PRIOR PELING DATE: 1999-06-03
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/10033301
Patent No. US20020098506A1
GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Stewart, Timothy A.
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 11
LENGTH: 325
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Ferrara, Napoleone
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Goddard, Audrey
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                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-033-246-11
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US-10-033-301-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2930R1C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-12-28
PRIOR PLICATION NUMBER: 05/095,325
PRIOR APPLICATION NUMBER: 60/095,325
PRIOR FLING DATE: 1998-08-04
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-16
PRIOR PLICATION NUMBER: 60/113,145
PRIOR PLICATION NUMBER: 60/113,145
PRIOR PLICATION NUMBER: 60/113,511
PRIOR APPLICATION NUMBER: 60/113,511
PRIOR PLING DATE: 1998-12-2
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115,733
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115,733
PRIOR APPLICATION NUMBER: 60/115,733
PRIOR APPLICATION NUMBER: 60/115,733
PRIOR APPLICATION NUMBER: 60/115,733
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R FILING DATE: 2000-02-11

R APPLICATION NUMBER: PCT/USO0/0414

R FILING DATE: 2000-02-22

NR APPLICATION NUMBER: PCT/USO0/05841

R FILING DATE: 2000 -03-02

NR APPLICATION NUMBER: PCT/USO0/08439

NR APPLICATION NUMBER: PCT/USO0/18439

NR APPLICATION NUMBER: PCT/USO0/18439

NR APPLICATION NUMBER: PCT/USO0/18439

NR FILING DATE: 2000-03-30

NR FILING DATE: 2000-05-30
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APPLICATION NUMBER: PCT/US99/12252
FILING DATE: 1999-06-02
APPLICATION NUMBER: PCT/US99/28634
FILING DATE: 1999-12-01
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PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/32678
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FILING DATE: 1999-12-02
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R APPLICATION NUMBER: 60/162,506
R FILING DATE: 1999-10-29
R APPLICATION NUMBER: 60/170,262
R FILING DATE: 1999-12-09
R APPLICATION NUMBER: 60/187,202
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APPLICATION WUMBER: 00/119,537
FILING DATE: 1999-02-10
APPLICATION NUMBER: 60/119,965
                                                                                                                                                                                                 Sequence 11, Application US/10033246 Patent No. US2002098505A1 GENERAL INFORMATION: APPLICANT: Botstein, David
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Stewart, Timothy A.
Tumas, Daniel
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                                      270 CPICKNGPNCFAETAVIP 287
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Gao, Wel-Qiang
Goddard, Audrey
Gurney, Austin L.
Pan, James
| 25 CSICSNNPTCWAICKRIP 42
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US-10-033-246-11
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us-uy-864-/61-48887

Sequence 48887, Application US/09864761

Sequence 48887, Application US/09864761

Sequence 48887, Application US/09864761

Sequence 48887, Application US/09864761

Septemation, Sharron G.

APPLICAWT: Penn, Sharron G.

APPLICAWT: Rank, David R.

APPLICAWT: Rank, David R.

APPLICAWT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENCME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR INVENTION: HUMAN GENCME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL CANT.

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acond-car x-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Pred. No. 38;
1; Mismatches 8; Indels
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170,262
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR PLICATION NUMBER: 6C/187,202
PRIOR PLICATION NUMBER: PCT/US99/1252
PRIOR PLILNG DATE: 1999-06-02
PRIOR PLILNG DATE: 1999-12-01
PRIOR PLILNG DATE: 1999-12-01
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 2000-02-11
PRIOR PLILNG DATE: 2000-02-11
PRIOR PLILNG DATE: 2000-02-12
PRIOR PLILNG DATE: 2000-02-13
PRIOR PLILNG DATE: 2000-03-02
PRIOR PLILNG DATE: 2000-03-02
PRIOR PLILNG DATE: 2000-03-02
PRIOR PLILNG DATE: 2000-03-03
PRIOR PLILNG DATE: 2000-05-30
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Best Local Similarity 50.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Pred. No. 38;
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                                 PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR PLICATION NUMBER: PCT/US00/08439
PRIOR PLICATION NUMBER: PCT/US00/14941
PRIOR PRIOR DATE: 2000-03-30
PRIOR PLILING DATE: 2000-05-30
PRIOR PLILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 38
TYPE: PRIOR PRIOR
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/095,325
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PRIOR APPLICATION NUMBER: 60/112,851
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113,145
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-2
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113,511
PRIOR APPLICATION NUMBER: 60/115,558
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PRIOR APPLICATION NUMBER: 60/115,565
PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119,537
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APPLICATION NUMBER: 60/119,965
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PRIOR FILING DATE: 1999-01-12
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50.0%;
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
Gurney, Austin L.
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                FILING DATE: 2000-02-11
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Matches 9; Conservative
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US-10-033-326-11
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL MOTITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISSPROT HIT: P14077, EVALUE 1.00e-09
EST_HUMAN HIT: AA668227.1, EVALUE 1.00e-34
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ED IN HELLOO, SIGNAL = 1.8

ED IN HERAT, SIGNAL = 1.2

ED IN BONE WARROW, SIGNAL = 1.5

ED IN BRAIN, SIGNAL = 0.91

ED IN LONG, SIGNAL = 1.6

ED IN ADULT LIVER, SIGNAL = 2.8

ED IN BTATA, SIGNAL = 0.99

ED IN FETAL LIVER, SIGNAL = 1.4

ED IN HELA, SIGNAL = 1.4
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SOCTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35081
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENE EARKESSION ANALISIS.
CURRENT APPLICATION NUMBER: US/09/664,761
CURRENT FILING DATE: 2001-05-23
PRIOR PEDILOCATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00665
PRIOR PAPLICATION NUMBER: PCT/USO1/00668
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                               Sequence 35081, Application US/09864761
Patent No. US20020048763A1
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EXPRESSED I
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EST_HUMAN HIT: BF220308.1, EVALUE 5.00e-16
OTHER INFORMATION: SWISSPROT HIT: P36627, EVALUE 4.30e-01
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PRIOR PLICATION NUMBER: PCT/USOL/UGORB
PRIOR PELICATION NUMBER: PCT/USOL/OG63
PRIOR PELICATION NUMBER: PCT/USOL/OG62
PRIOR PELICATION NUMBER: PCT/USOL/OG62
PRIOR PELICATION NUMBER: PCT/USOL/OG61
PRIOR PELICATION NUMBER: PCT/USOL/OG61
PRIOR PELICATION NUMBER: PCT/USOL/OG60
PRIOR PELICATION NUMBER: PCT/USOL/OG60
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PELICATION NUMBER: US 09/608,408
PRIOR PELICATION NUMBER: US 09/774,203
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Pred. No. 4.3;
7; Mismatches 16;
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4; Mismatches
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APPLICANT: Wong, James F.
TITLE OF INVENTION: SCORPION TOXINS
TITLE REFERENCE: BB1367 US NA
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICTOSOFT Office 97
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Pred. No. 8
                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
APPLICATION NUMBER: PCT/US01/00665
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Patent No. US20020160454A1
GENERAL INFORMATION:
APPLICANT: HERTMAN, Rafael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 CSNNPTCWAICKRIPNKKPGK 48
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26.1%;
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; ORGANISM: Hottentotta judaica
US-10-044-359-16
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Best Local Similarity 33.3%;
Matches 7; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 58
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DB 10; Length 102; 17.4%; Score 50;

Query Match

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381 KONN-----FNAVRCSHYPNHPLWYTLCDR 405

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Search completed: November 22, 2002, 14:30:23 Job time: 12 secs
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APPLICANT: Gee, Melissa
APPLICANT: Tilotson, Bonnie
APPLICANT: Chang, Xiao-Jia
APPLICANT: Chang, Xiao-Jia
APPLICANT: Chang, Xiao-Jia
TITLE OF INVENTION: Receptor and Orphan Receptor Function Using Reporter
TITLE OF INVENTION: Enzyme Mutant Complementation
TITLE OF INVENTION: Enzyme Mutant Complementation
FILE REFERENCE: 4085-235-27 CIP
CURRENT APPLICATION NUMBER: US/09/759,152
CURRENT APPLICATION NUMBER: US 09/654,499
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/180,669
PRIOR FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 9
SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 1010
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                             16;
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                             Indels
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US-09-879-257A-30
Sequence 30, Application US/09879257A
Fatent No. US20020081690A1
GENERAL INFORMATION:
APPLICANT: VAMAMOTO, SACHIKO
APPLICANT: HANADA, TOSHIRO
APPLICANT: HANADA, TOSHIRO
APPLICANT: HANADA, TOSHIRO
APPLICANT: HANBO, MINORU
APPLICANT: HANBO, MINORU
APPLICANT: HANBO, MINORU
CHERENT: SHIRO
FILE REPERBNCE: 55986/70281)
CURRENT APPLICATION UNBER: US/09/879,257A
CURRENT FILLING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 1024
TYPE: PRT
COGANISM: ESCHETICHIA COli
US-09-879-257A-30
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30.0%; Pred. No. 15; tive 4; Mismatches
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Patent No. US20020028433A1
GENERAL INFORMATION:
APPLICANT: Palmer, Michelle A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
FEATURE:
COHEN INFORMATION: PICAST ALC.
US-09-759-152-2
  Best Local Similarity 30.09
Matches 12; Conservative
                                                                                                                                                                                       RESULT 14
US-09-759-152-2
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RESULT 2
US-08-467-963C-8
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53, Appli
13, Appl
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                                                                                                     November 22, 2002, 14:25:06; Search time 15 Seconds (without alignments) 96.115 Million cell updates/sec
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Compugen Ltd
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US-08-852-344D-8
US-08-467-965A-8
US-08-467-961A-8
US-08-01-554A-8
US-08-793-792-8
US-08-793-792-4
US-08-793-792-4
US-08-793-792-4
US-08-793-792-11
US-08-793-792-11
US-08-793-792-7
US-08-836-504A-6
US-08-836-504A-5
US-08-836-504A-5
US-08-836-504A-5
US-08-793-792-13
US-08-793-792-13
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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-09-654-289-9
                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
      GenCore version Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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288
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                       Sequence:
                                                                                                        Run on:
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No.
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Patent No. 5968776
GENERAL INFORMATION:
APPLICANT: Michel H
APPLICANT: DV, Nun-Pan
APPLICANT: DV, Nun-Pan
APPLICANT: EMASYSHYN, MAIY
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTECT WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
                                                            Appl
Appli
Appli
Appli
Appli
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Appli
Appli
                            Sequence 20, Sequence 20, Sequence 1, P. Sequence 1, P. Sequence 19, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 8, P. Sequenc
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; TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
; TIMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
; SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 288; DB 6; Best Local Similarity 100.0%; Pred. No. 1.7e-26; Matches 49; Conservative 0; Mismatches 0;
US-08-721-979A-20

US-08-836-501-20

US-08-654-289-20

US-08-793-792-1

US-08-793-792-9

US-08-793-792-9

US-08-793-792-9

US-08-771-979A-19

US-08-836-501-19

US-09-654-289-11

US-08-836-501-11

US-09-654-289-11

US-08-656-055-8

US-08-656-055-8

US-08-951-668-8

US-08-918-668-8

US-08-918-668-8

US-08-918-668-8
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6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/543,780
FILING DATE: 31-OCT-1988
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 137,387
FILING DATE: 23-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim 6
STREET: 6th Floc
CITY: Toronto
STATE: Ontario
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     Patent No. 5194595
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5194595-19
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Gaps
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APPLICANT: DU, Run-Pan
APPLICANT: EWASYSHYN, Maxy
TITLE OF INVENTION: CHIMBERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                              Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKFGKK 197
                                                                                                                                                                                                                                                                                                                                                                                         1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JULIANARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
'RIOR APPLICATION: 424
                                                                                                                                                                                                                                                                                            Score 285; DB 2;
Pred. No. 1.7e-26;
1; Mismatches 0
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Pred. No. 1.7e-26;
24,973
ER: 1038-687 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6th Floor, 330 University
CITY: Toronto
STAME: Ontario
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIABLE
COMPUTER: PATENTIS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08852344D Patent No. 6017539
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
TELEPHONE: (416) 595-1163
TELEPHONE: (416) 595-1163
FELEPHONE: (416) 595-1163
TELEPHONE: (416) 595-1163
TELEPHONE OF REACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
US-08-838-189D-8
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              99.08;
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98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.08
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-852-344D-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-852-344D-8
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APPLICANT: EWASYSHXN, MAIY E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: GITMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
PROPER SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKFGKK 197
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SOFTWARE: Patentin Release #1.0, Version #1.30
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                               1038-474 MIS: jb
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APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
| CLASSIFICATION: 435
| RICHARD APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
| FILING DATE: 06-JAN-1993
| PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
PRILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08838189D Patent No. 5998169
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: DU, RUN-Pan
APPLICANT: EWASYSHYN, MATY E
                                                                                                                                                                                                                                                                                                              | NAME: STEWART, MICHAELI
| REGISTRATION NUMBER: 24,973
| REFERENCE/DOCKET NUMBER: 1038
| TELECOMMUNICATION INFORMATION:
| TELEFAN: (416) 595-1155
| TELEFAX: (416) 595-1153
| INFORMATION FOR SEO ID NO: 8:
| SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEWART, Michael I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: Canada
ZIP: M5G 1R7
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       Gaps
                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 99.0%; Score 285; DB 3; Length 298; Best Local Similarity 98.0%; Pred. No. 1.7e-26; Matches 48; Conservative 1; Mismatches 0; Indels
                                           149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
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    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: MSG 1M/
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: U-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1993
CLASSIFICATION A24
PRIOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
TELEROMORICATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S99-1155
TELEFRA: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEGUIBNE EGRRACERRISTICS:
TENTATH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATIO Ontario
STATIO COUNTRY: Canada
ZIP: M5G 1R7
  1; Mismatches
                                                                                                                                                                                                         Sequence 8, Application US/08344639E
Patent No. 6033668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08467969A Patent No. 6168786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-639E-8
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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US-08-467-969A-8
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  Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 KORONKPPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                        ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08467961A
Patent No. 6171783
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chlmeric Immunogens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6TH Floor
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION 1435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 298 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
                                                                                                                                                        CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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TITLE OF INVENTION: Antigenic peptides derived from the TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection. NUMBER OF SEQUENCES: 13 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
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                                                                                                                                                                                                                                                                                                        Length 298,
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                                                                                                                                                                                                                                                                                                                                                                                                1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                   Score 285; DB 4; La
Pred. No. 1.7e-26;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 217; DB 3;
Pred. No. 2.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 SKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
TITLE OF INVENTION: Antigenic pr
TITLE OF INVENTION: G-protein of
TITLE OF INVENTION: of respirate
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                       TELEPHONE: (416) 595-1155
TELEFA: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                   Query Match 99.0%;
Best Local Similarity 98.0%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.3%;
Best Local Similarity 97.3%;
Matches 36; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
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                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                             TOPOLOGY: 1 MOLECULE TYPE:
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US-08-793-792-12
                                                                                                                                                                                                                                                             US-08-001-554A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
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                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
MAPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08001554A
Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: ELSON MICHEL H
APPLICANT: Du. Run-Pan
APPLICANT: EMASYSHYN, MARY E
TILE OF INFORMATION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: TOTONTO
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                         | FILING DATE: 06-JUN | CLASSIFICATION: 435 | PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/001,554 | FILING DATE: 06-JAN-1993 | CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION: APPLICATION: APPLICATION: APPLICATION:
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NAME: Stewart, michael I
REGISTRATION NUMBER: 24,913
REFERENCE/DOCKET NUMBER: 1038-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 595-1155
TELERA: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
COMPUTER READABLE FORM:
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: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-467-961A-8
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APPLICANT: James, Olive A
APPLICANT: James, Olive A
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
TITLE OF INVENTION: ADJUVANT COMPOSITIONS COMPRISING A
TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.7%; Score 146; DB 4; Length 26; 100.0%; Pred. No. 4.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 151; DB 3;
Pred. No. 1.6e-11;
4; Mismatches ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KPKDDYHFEVFWFVPCSICGNNQLCKSICKTIPSNK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sim & McBurney .
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/750,624
26-FEB-1997
                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08750624
Patent No. 6290971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEC ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.4%;
Best Local Similarity 69.4%;
Matches 25; Conservative
                                                                                                                                                                                  CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-793-792-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kandil, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontari
COUNTRY: Cana
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Antigenic peptides derived from the TITLE OF INVENTION: G-protein of RSV for type- and subtype TITLE OF INVENTION: G-protein of RSV for type- and subtype TITLE OF INVENTION: of respiratory syncytial virus (RSV) NUMBER OF SEQUENCES: 13 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SYSTEM: PC-DSYMS-DOS SOFTWARE: Patentin Re-base #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 28;
                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.0%; Score 193; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 32
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Patent No. 6077511
GENERAL INFORMATION:
TITLE OF INVENTION: G-protein of RE, TITLE OF INVENTION: G-protein of RE, TITLE OF INVENTION: Of respiratory NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                        INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 32 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
  OPERATING SYSTEM:
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                                                                                          FILING DATE:
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US-08-793-792-11
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                   APPLICANT: Binz, Hans
APPLICANT: Nguyen Ngoc, Thien
APPLICANT: Stain.
APPLICANT: Stain.
APPLICANT: Uhlen, Mathias
APPLICANT: Nygren, Per Ake
TITLE OF INVENTION: Method for obtaining a peptide derived
TITLE OF INVENTION: from the respiratory syncytial virus, polypeptide and
TITLE OF INVENTION: medicinal product.
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89.7%; Pred. No. 6.6e-11;
.ive 0; Mismatches 3; Indels
  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Rockey, Milnamow & Katz
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/836,504A
FILING DATE: 07-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIE1514P0200US
TELEPHONE: 312-616-5400
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 NFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antigenic pept
TITLE OF INVENTION: G-protein of i
                                 1 KORQNKPPSKPNNDFHFEVFNFVPC 25
                                                         2 KQRQNKPPSKPNNDFHFEVFNFVPC 26
                                                                                                                                                                             Sequence 6, Application US/08836504A Patent No. 6130091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-616-5460 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 30 amino acids TYPE: amino acid
25; Conservative
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COMPUTER READABLE FORM:
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TOPOLOGY: line
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US-08:836-504A-6
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US-08|-793-792-7
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  Matches
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: PatentIN Release #1.0, Version #1.30 (EPO)

COMPUTER: PatentIN Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,792

FILING DATE:

CLASSTRICATION: 514

INFORMATION FOR SED ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino ac
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(without alignments)
186.551 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*

/SIDS2/gcgdata/geneseq/genesegp-embl/AA1996. /SIDS2/gcgdata/geneseq/genesegp-embl/AA1997.

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*

/SIDS2/gcgdata/geneseq/genesegp-emb1/AA1991. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1992.

## SUMMARIES

(BIOM-) BIOMOLECULAR RES INST LTD.

WPI; 1998-042117/04

Gorman JJ;

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Human RSV A subtyp Respiratory Synoyt RSV G protein anti Amino acid sequenc Respiratory Synoyt RSV G protein anti	ubgroup ubgproup ubgproup protection acid acid acid acid acid acid acid acid	он	. 149-157) strain A2. s; infection; immunity; cine; cell receptor.	
AAW39218 AAW39219 AAW39221 AAW39222 AAW39223 AAW39224 AAK97073 AAK91100 AAR97073 AAK97073 AAK97073	AAR88213 AAR88213 AAR85616 AAR95616 AAR97050 AAX44078 AAB68016 AAB68016 AAB68016 AAB68016 AAR39286 AAR39286 AAR39280 AAR95660 AAR95660 AAR95660 AAR95660 AAR97071 AAR97074	AAN97311 AAR97075 AAY44102 ALIGNMENTS 49 AA.	<pre>try) protein fragment (aa. prevention; diagnosis identification; vacc ytial virus. on/Qualifiers</pre>	
201120000000000000000000000000000000000	79111777777777777777777777777777777777	20 20 20 30 30	try) protein prevent identi ytial v	351.
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	00000000000000000000000000000000000000	· · · ·	(first subtype reatmen eumovir atory s atory s ond 25.	நெ
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49 AA;
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                                                                            Sequence
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Matches
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                                                            AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          5 protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
Peptide(s) derived from specific region of respiratory syncytial virus G protein – used to treat, prevent, diagnose and immunise
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                Length 49;
                                                                                                                                                                                                                                         Human RSV G protein fragment (aa. 149-157) derivative #1.
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Pred. No. 2.2e-28;
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                                                                                                                                                                                                                                                                                                                    AAW39244 standard; peptide; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus.
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                                                                                                                                                                                              100.0%;
            virus G protein – used to trea
against Pneumovirus infection
                                          Claim 5; Fig 2; 75pp; English.
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                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
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                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                          49 AA;
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                                                                                                                                                                                                                                                                                                                                           AAW39244;
                                                                                                                                                                          Sequence
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                           AAW39244
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infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein; treatment; prevention; diagnosis; infection; immunity;
antibody; Pneumovirus; identification; vaccine; cell receptor.
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                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human RSV G protein fragment (aa. 149-157) derivative #5.
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                     ; DB 19;
2.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-terminal fitc group"
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                  Score 288;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus.
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                                                                                                                                                                                                                                                                                                                  100.0%; S
llarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW39248 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-AU00351
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                49 AA;
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Disulfide-bond
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Human RSV G protein fragment (aa. 149-157) derivative #8.
                                             AAW39251 standard; peptide; 49
                                                                                                                            27-AUG-1998 (first entry)
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                                                                                      AAW39251;
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                        AAW39251
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                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.
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  Length 49;
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                                                                                                             1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                      1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                       Human RSV G protein fragment (aa. 149-157) derivative #7.
                                             Indels
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llarity 100.0%; Pred. No. 2.2e-28;
Conservative 0; Mismatches 0;
Score 288; DB 19;
Pred. No. 2.2e-28;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-terminal bb group"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 12; 75pp; English.
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                                                                                                                                                                                                                                          AAW39250 standard; peptide; 49
100.0%;
100.0%;
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                                             49; Conservative
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25..38
28..34
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                      Similarity
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es 49; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                  AAW39250;
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  Query Match
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Matches
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AAW39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used confortify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
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diagnosis; infection; immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
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                             antibody; Pneumovirus; identification; vaccine; cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 49;
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nilarity 100.0%; Pred. No. 2.2e-28;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                'note= "N-terminal biot group"
                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                       Location/Qualifiers
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                                                                                  Human respiratory syncytial virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-AU00351
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                                                                                                                                                                                                                          25..38
28..34
  protein; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-042117/04.
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                             Key
Modified-site
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The sequences of mRNA encoding HRSV structural proteins are given in AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences are effect proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production of human respiratory syncytial virus glyco-protein F or (- by culturing eukaryotic host cells transfected with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for the production of human respiratory syncytial virus (HRSV) glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare vaccines against HRSV.
                                                                                                                                                                                            immunity against respiratory tract infections on human subjects.
                                                                                                                                                                                                                                                          Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the development of a novel
                              Vaccines for human respiratory virus – include structural ge coding for native structural viral proteins and immunogenic
                                                                                                                                                                                                                                                                                                                                          149 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKK 197
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
                                                                                                                                                                                                                                                                                                                           1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
                                                                                                                                                                                                                                                        Score 288; DB 13;
Pred. No. 1.4e-27;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Columns 27-28; 17pp; English.
                                                                                              Disclosure; Page 18; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW47605 standard; Protein; 298
                                                                                                                                                                                                                                                          ch 100.0%; S
1 Similarity 100.0%; P
49; Conservative 0;
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92US-0897171.
97US-0854783.
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86US-0818740.
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                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                             298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRSV glycoprotein
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N-PSDB; AAQ29623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5716823-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins PL,
                                                                 fragments
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW47605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                           Matches
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Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K; major capsid protein; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV yaccines. The vaccine can be administered to pregnant women or women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age.
                                                                                                                                                                                                                                                                                                                                       Paccines for human respiratory virus - comprising proteins or fragment encoded by a DNA sequence coding for human respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 288; DB 8;
ilarity 100.0%; Pred. No. 1.4e-27;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus strain A2
                                                              !uman respiratory syncytial virus (HRSV).
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Chart 13; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR25302 standard; Protein; 298
                                                                                                                                                          86WO-US02756
                                                                                                                                                                                          86US-0818740
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                                                                                                                                                                                                                       (UYNC-) UNIV OF N CAROLINA.
(WERT/) WERTZ G W.
(WERT/) WERTZ G W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSRV glycoprotein G (gpG).
                                                                                                                                                                                                                                                                                                                                                                          syncytial virus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wertz GW;
                                                                                                                                                                                                                                                                                        WPI; 1987-206300/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-340247/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AA;
                                                                                                                                                                                                                                                                                                           N-PSDB; AAN70784.
                                                                                                                                                            3-DEC-1986;
                                                                                                                                                                                          4-JAN-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-1986;
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                                                                                          WO8704185-A
                                                                                                                            16-JUL-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                              /accine.
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Matches
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suitable for expression by the recombinant virus of the invention.

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comprising nucleic acid encoding a paramyzovirus (PMV) protein or its antigenic fragment. The virus may be administered in combination with an antifyrial chemotherapeutic compound. Two or more viruses expressing different PMV proteins nay be administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendal virus comprising an exogenous nucleic acid encoding a second PMV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendal viral vector encoding a PMV protein. The recombinant virus is useful as an effective vaccine against hipty or RSV (the major causes of paediatric respiratory disease) and also to express any gene of interest in target cells, providing a positive medical impact on into stem cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathal sasammia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The sendal virus replicates at level that is high enough to human recipient. The present sequence represents a respiratory syncytial virus RSV) G protein (heavily glycosylated protein), a PMV protein
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                                                                                                                                                                                                                                                                                                                                                                                                              protein; heavily glycosylated protein; antianaemic; antiviral;
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Sendal virus useful in vaccines to protect infection by paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a recombinant Sendai virus comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; gene therapy; paramyxovirus; sendai virus; PWV; antiviral chemotherapeutic compound; humoral response; cellular immune response; hPV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
                                             ö
Length 298;
                                                                                                          149 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKK 197
                                                                                   1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                             Indels
  DB 19;
                      1.4e-27
                                        0; Mismatches
100.0%; Score 288; 100.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                       Respiratory syncytial virus G protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 48; 57pp; English.
                                                                                                                                                                                                                                      AAU74676 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-2001; 2001WO-US16610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000; 2000US-208701P.
                                                                                                                                                                                                                                                                                                                            (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Portner A, Takimoto T;
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N-PSDB; AAS21045.
                      Similarity
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                                        49;
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Query Match
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Matches
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                                                                     Gaps
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                                                                                                                                                                                                                                                          Chimeric human respiratory synctial virus glycoproteins F and G.
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                                              Length 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric human respiratory syncytial virus polypeptides(s) - contg. immunogenic fragments from HRSV glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 591
                                                                                                          149 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                     Indels
                                                                                                                                                                                                                                                                             Chimeric polypeptide; human respiratory syncytial virus; protein F; protein G; vaccine.
                                                                                              1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
                                           ; Score 288; DB 23;
; Pred. No. 1.4e-27;
0; Mismatches 0;
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100.0%; Pred. No. 3.
ive 0; Mismatches
                                                                                                                                                                                 681 AA
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                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW39218 standard; peptide; 49
                                              100.0%;
100.0%;
                                                                                                                                                                                AAP90441 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                              88WO-US03784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F and G, for vaccine prodn
                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Conservative
                                                                      Conservative
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Best Local Similarity
Matches 49; Conserv
                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 AA;
                     298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (UPJO ) UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. frugiperda.
                                                                                                                                                                                                                                 01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1987;
                                                                                                                                                                                                                                                                                                                                               WO8905823-A.
                                                                                                                                                                                                                                                                                                                                                                      29-JUN-1989
                                                                      49;
                                                                                                                                                                                                          AAP90441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wathen M;
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                       Sequence
                                             Query Match
                                                                      Matches
                                                                                                                                                         RESULT 10
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AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human RSV A subtype G protein fragment (aa. 149-157) strain A6256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; treatment; prevention; diagnosis; infection; immunity;
                                                                                                                                                                                                                                     Peptide(s) derived from specific region of respiratory syncytial virus G protein – used to treat, prevent, diagnose and immunise against Pneumovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide(s) derived from specific region of respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; Pneumovirus; identification; vaccine; cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 285; DB 19;
Pred. No. 5.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
25..38
28..34
                                                                                                                     LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                   (BIOM-) BIOMOLECULAR RES INST
                                                                                                                                                                                                                                                                                                                Claim 5; Fig 2; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%;
98.0%;
                                      97WO-AU00351
                                                                             96AU-0000265
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                                                                                                                                                                                            WPI; 1998-042117/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                      04-JUN-1997;
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                                                                           05-JUN-1996;
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11-DEC-1997
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                                                                                                                                                            Gorman JJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used conhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Human RSV A subtype G protein fragment (aa 149–157) strain long A.
                                      G protein; treatment; prevention; diagnosis; infection; immunity;
antibody; Pneumovirus; identification; vaccine; cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; treatment; prevention; diagnosis; infection; immunity;
intibody; Pneumovirus; identification; vaccine; cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human RSV A subtype G protein fragment (aa. 149–157) strain A642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
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Pred. No. 5.3e-28;
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98.08;
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28..34
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Sequence

Query Match

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may allow a reduction in dose, and thus side effects, of the vaccine
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                                                            AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
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 virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
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Pred. No. 5.3e-28;
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                                    Claim 5; Fig 2; 75pp; English.
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against Pneumovirus infection
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Disulfide-bond
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antibody; Pneumovirus; identification; vaccine; cell receptor
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Pred. No. 5.3e-28;
                                        Score 285; DB 19;
Pred. No. 5.3e-28;
1; Mismatches 0;
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49 AA;
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